-114

SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Klein, Theodore M.
Odell, Joan T.
Orozco, Emil M. Jr.

<120> PLANT CELL CYCLIN GENES

<130> BB1149 US NA

<140> US/09/665,308
<141> 2000-09-19

<150> 60/078,735
<151> 1998-03-20

<150> PCT/US99/06047
<151> 1999-03-19

<160> 32

<170> MICROSOFT OFFICE 97

<210> 1
<211> 1071
<212> DNA
<213> Zea mays

<400> 1
ccggaattcc cggggtcgac ccacgcgtcc ggccgcgcgc cgtggcgccc gccgacctcc 60
agctctccgg gtcctacgcc tccgacatct acacctacct ccgctccctg gaggtggatc 120
cgcagcggcg gtccagatcc gattacatcg aggcggtgca ggcggacgtc acggcccaca 180
tgcggagcat cctcgtcgac tggctcgtcg aggtcgccga ggagtacaag ctcgtcgcgg 240
acacgctcta cctcaccatc tcttatgtcg accgcttcct ctccgtcaac gcgctcggcc 300
gtgacaagct gcagctcctt ggcgttgcct ccatgctcat tgccgcgaag ttcgaggaga 360
tcagcccgcc gcacccggag gacttctgct acatcacaga caacacctac accaaagagg 420
agctcctcaa gatggagagc gacatactca agcttctcaa gttcgagttg ggcaatccta 480
caatcaagac cttcctgaga cgtttcataa gatctgccca tgaagacaag aagggctcca 540
tcttgttaat ggaattcttg gggagctacc tcgctgagct gagtctacta gattatggct 600
gcctccggtt cttgccatca gtagttgctg cttcagtcat gtttgttgct aggcctgaca 660
ttgatccaaa taccaatccg tggaacacaa agctgcagaa gatgactggc tacaaagttt 720
ctgaactcaa ggattgcatc gtagccatac atgacttgca gctcaacagg aaatgtccat 780
cattaacggc aattcgagac aagtacaagc agcacaagtt caaatgcgtg tcattgatcc 840
tcgtgcctgt cgtgatccct acttcatact ttgaagactt agctgagtag ctgctctcgg 900
actgtaccgc tgtaaggcta acaatctgag ctctccttga gctcttaggg acaagcagaa 960
aataaccgtt tgatgagctt tcctctcatt taagtagcgt ggtgaaagct atttgtttga 1020
ggttctttag gattaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1071

<210> 2
<211> 295
<212> PRT
<213> Zea mays

<400> 2
Gly Ile Pro Gly Val Asp Pro Arg Val Arg Pro Arg Ala Val Ala Pro
1 5 10 15

Ala Asp Leu Gln Leu Ser Gly Ser Tyr Ala Ser Asp Ile Tyr Thr Tyr
20 25 30

Leu Arg Ser Leu Glu Val Asp Pro Gln Arg Arg Ser Arg Ser Asp Tyr
35 40 45

Ile Glu Ala Val Gln Ala Asp Val Thr Ala His Met Arg Ser Ile Leu
50 55 60

Val Asp Trp Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Val Ala Asp
65 70 75 80

Thr Leu Tyr Leu Thr Ile Ser Tyr Val Asp Arg Phe Leu Ser Val Asn
85 90 95

Ala Leu Gly Arg Asp Lys Leu Gln Leu Leu Gly Val Ala Ser Met Leu
100 105 110

Ile Ala Ala Lys Phe Glu Glu Ile Ser Pro Pro His Pro Glu Asp Phe
115 120 125

Cys Tyr Ile Thr Asp Asn Thr Tyr Thr Lys Glu Glu Leu Leu Lys Met
130 135 140

Glu Ser Asp Ile Leu Lys Leu Leu Lys Phe Glu Leu Gly Asn Pro Thr
145 150 155 160

Ile Lys Thr Phe Leu Arg Arg Phe Ile Arg Ser Ala His Glu Asp Lys
165 170 175

Lys Gly Ser Ile Leu Leu Met Glu Phe Leu Gly Ser Tyr Leu Ala Glu
180 185 190

Leu Ser Leu Leu Asp Tyr Gly Cys Leu Arg Phe Leu Pro Ser Val Val
195 200 205

Ala Ala Ser Val Met Phe Val Ala Arg Pro Asp Ile Asp Pro Asn Thr
210 215 220

Asn Pro Trp Asn Thr Lys Leu Gln Lys Met Thr Gly Tyr Lys Val Ser
225 230 235 240

Glu Leu Lys Asp Cys Ile Val Ala Ile His Asp Leu Gln Leu Asn Arg
245 250 255

Lys Cys Pro Ser Leu Thr Ala Ile Arg Asp Lys Tyr Lys Gln His Lys
260 265 270

Phe Lys Cys Val Ser Leu Ile Leu Val Pro Val Val Ile Pro Thr Ser
275 280 285

Tyr Phe Glu Asp Leu Ala Glu
290 295

<210> 3
<211> 435
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (86)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (88)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (216)..(217)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (231)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (240)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (307)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (372)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (377)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (427)
<223> n = A, C, G or T

<400> 3
nactccatct tcttccatcc atttcctctt tctcgatctg ttccaaattc acttcacaca 60
caggaaagaa gatggagact cgcgcngncg caaagagaaa ggcaaatgcc gccaccatag 120
tctttgtcga aaaacaatac cccaacaaga ggcagcgggt tgtgttgggt gaacttccca 180
atttacaaaa ccttattgtc tccgaaactc aaaatnngcg caaagagaag ntcctatgtn 240
ggaagaatcc caatgagaag aaaccatcac ccacaaacaa caacaccttt ccttcccctc 300
agatcancga atcttatgat tcggatatcc acgggtatct tcgtgaaatg gagatgcaga 360
ataagagaag ancaatngtt gatacattga aaaggttaga aaatcgttac ccaaccatgg 420
agcaatntgg tgatt 435

<210> 4
<211> 110
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (6)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (49)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (54)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (57)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (79)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (101)..(102)
<223> Xaa = ANY AMINO ACID

<400> 4

```
Met Glu Thr Arg Ala Xaa Ala Lys Arg Lys Ala Asn Ala Ala Thr Ile
1               5                  10                  15

Val Phe Val Glu Lys Gln Tyr Pro Asn Lys Arg Gln Arg Val Val Leu
            20                  25                  30

Gly Glu Leu Pro Asn Leu Gln Asn Leu Ile Val Ser Glu Thr Gln Asn
        35                  40                  45

Xaa Arg Lys Glu Lys Xaa Leu Cys Xaa Lys Asn Pro Asn Glu Lys Lys
    50                  55                  60

Pro Ser Pro Thr Asn Asn Asn Thr Phe Pro Ser Pro Gln Ile Xaa Glu
65                  70                  75                  80

Ser Tyr Asp Ser Asp Ile His Gly Tyr Leu Arg Glu Met Glu Met Gln
                85                  90                  95

Asn Lys Arg Arg Xaa Xaa Val Asp Thr Leu Lys Arg Leu Glu
            100                 105                 110
```

<210> 5
<211> 847
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (584)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (686)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (704)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (731)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (748)

<223> n = A, C, G or T

<220>
<221> unsure
<222> (768)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (772)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (781)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (785)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (803)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (806)..(807)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (819)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (825)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (830)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (839)
<223> n = A, C, G or T

<400> 5
cggaacaggg agagtggtgt tcatgagcca ttctttcagg gaagaaacac aagagataaa 60
tctgaaactg ctgactcaaa cactgggtac tatgttggct taaacgttat agacattgac 120
aaagataatg gcaatccaca aatgtgtgct tcctatgctg cagagatata cagaaaccta 180
atggctgcag agcttataag gagacctaaa tcaaattaca tggagacttt gcaaagggat 240
atcacaaagg gcatgcgagg aatcctgatt gattgggctt tgaggttcct ggaggaatat 300
aaacttttgc cagacacact atacctcact gtatatctta ttgatcaatt tctttctcgg 360
aaatatattg aaagacagaa actacaactt cttggaataa ctagcatgct gattgcctca 420
aaatatgaag agatctgtgc gcctcgtgtt gaagaatttt gtttcataac tgataacaca 480
tatacaaaaa atcaggtgct gaaaatggag tgtgaagtgc ttaatgatct ggggtttcat 540
ctttcagttc ccacaatcaa aacgtttctg aggagattcc ttanagcagc acatgcttct 600
caaaaaagcc cttgggcaac tttgggctat ctggggcaat tatcttgccg gagttgacat 660
tgaccgatta cagttccctg aaattnaacc tcaatgggtg gaanctcggc gggtccctgc 720
aaaatggcac ncgacatcag actgcaangg aatccacctc gagcatanac tnaatcaaaa 780

nttangtatc aagatgcgta cgnatnnatg gaactgacna ggaanacaan ggatccccna 840
aggtata 847

<210> 6
<211> 211
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (195)
<223> Xaa = ANY AMINO ACID

<400> 6

Arg	Asn	Arg	Glu	Ser	Gly	Val	His	Glu	Pro	Phe	Phe	Gln	Gly	Arg	Asn
1				5				10						15	
Thr	Arg	Asp	Lys	Ser	Glu	Thr	Ala	Asp	Ser	Asn	Thr	Gly	Tyr	Tyr	Val
			20					25					30		
Gly	Leu	Asn	Val	Ile	Asp	Ile	Asp	Lys	Asp	Asn	Gly	Asn	Pro	Gln	Met
		35					40					45			
Cys	Ala	Ser	Tyr	Ala	Ala	Glu	Ile	Tyr	Arg	Asn	Leu	Met	Ala	Ala	Glu
	50					55					60				
Leu	Ile	Arg	Arg	Pro	Lys	Ser	Asn	Tyr	Met	Glu	Thr	Leu	Gln	Arg	Asp
65					70					75					80
Ile	Thr	Lys	Gly	Met	Arg	Gly	Ile	Leu	Ile	Asp	Trp	Ala	Leu	Arg	Phe
				85					90					95	
Leu	Glu	Glu	Tyr	Lys	Leu	Leu	Pro	Asp	Thr	Leu	Tyr	Leu	Thr	Val	Tyr
			100					105					110		
Leu	Ile	Asp	Gln	Phe	Leu	Ser	Arg	Lys	Tyr	Ile	Glu	Arg	Gln	Lys	Leu
		115					120					125			
Gln	Leu	Leu	Gly	Ile	Thr	Ser	Met	Leu	Ile	Ala	Ser	Lys	Tyr	Glu	Glu
	130					135					140				
Ile	Cys	Ala	Pro	Arg	Val	Glu	Glu	Phe	Cys	Phe	Ile	Thr	Asp	Asn	Thr
145					150					155					160
Tyr	Thr	Lys	Asn	Gln	Val	Leu	Lys	Met	Glu	Cys	Glu	Val	Leu	Asn	Asp
				165					170					175	
Leu	Gly	Phe	His	Leu	Ser	Val	Pro	Thr	Ile	Lys	Thr	Phe	Leu	Arg	Arg
			180					185					190		
Phe	Leu	Xaa	Ala	Ala	His	Ala	Ser	Gln	Lys	Ser	Pro	Trp	Ala	Thr	Leu
		195					200					205			
Gly	Tyr	Leu													
	210														

<210> 7
<211> 1007
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (924)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (958)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (971)..(972)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (996)
<223> n = A, C, G or T

<400> 7
gggagggaat tccttcctcc ttttctgttc ggcgccgtgc tcgcgcgcac ccacccgcac 60
gccccagtac ccccacgctg cacagtgcac gccgactttc ctccgccttg ctgctgcaag 120
tccgcaacca ctggaggaaa aatcttttcc ttcacttttc ttccctttcc ccccgcgcat 180
gcacgggctc tgattgacgc catgggggac gccgcggcct ccacgtccgc tcccaccacg 240
cccacctcca tcctcatctg cctggaagac ggcagcgacc ttctcgccga tgccgacgat 300
ggcgccggca ctgacctcgt tgtcgcccgc gacgaacgtc tgcttgtcgt ggaccaggac 360
gaggagtatg tagcgctgct cctgtccaag gagagcgcgt caggcggcgg cggcccggtg 420
gaggaaatgg aggactggat gaaggccgcg cgctccggat gcgtccgctg gatcatcaag 480
accacggcga tgttccggtt cggcgggaag accgcttacg tggccgtgaa ttacctcgat 540
cgcttcctgg cgcaacggcg agtcaatagg gagcatgcgt ggggtctgca gctgctcatg 600
gtggcgtgca tgtcgctggc gaccaagctg gaggagcacc acgctccgcg gctgtcggag 660
ttcccgctgg acgcgtgcga gttcgcgttc gacagcgcgt ccatcctgcg gatggagctc 720
ctcgtcctgg gcaccctcga gtggcggatg atcgccgtca ccccccttccc ctacatcagc 780
tacttcgcgg cgcggttccg ggagacgagc gccgggcgaa tcctcatgcg cgccgtggag 840
tgcgtcttcg cggcgatcaa agtgataagc tcggtggagt aacggccgtc gaccatcgcc 900
gtggcatcca tcctcgtcgc gcgnggccgg gaggagactc ccgccggcag cctgggangc 960
gctcaaggcg nntcctcggg tcatcgtgcc cgcaantaga aaacggg 1007

<210> 8
<211> 238
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (227)
<223> Xaa = ANY AMINO ACID

<400> 8
Met Gly Asp Ala Ala Ala Ser Thr Ser Ala Pro Thr Thr Pro Thr Ser
1 5 10 15

Ile Leu Ile Cys Leu Glu Asp Gly Ser Asp Leu Leu Ala Asp Ala Asp
20 25 30

Asp Gly Ala Gly Thr Asp Leu Val Val Ala Arg Asp Glu Arg Leu Leu
35 40 45

Val Val Asp Gln Asp Glu Glu Tyr Val Ala Leu Leu Leu Ser Lys Glu
50 55 60

Ser Ala Ser Gly Gly Gly Gly Pro Val Glu Glu Met Glu Asp Trp Met
65 70 75 80

Lys Ala Ala Arg Ser Gly Cys Val Arg Trp Ile Ile Lys Thr Thr Ala
85 90 95

Met Phe Arg Phe Gly Gly Lys Thr Ala Tyr Val Ala Val Asn Tyr Leu

100 105 110

Asp Arg Phe Leu Ala Gln Arg Arg Val Asn Arg Glu His Ala Trp Gly
115 120 125

Leu Gln Leu Leu Met Val Ala Cys Met Ser Leu Ala Thr Lys Leu Glu
130 135 140

Glu His His Ala Pro Arg Leu Ser Glu Phe Pro Leu Asp Ala Cys Glu
145 150 155 160

Phe Ala Phe Asp Ser Ala Ser Ile Leu Arg Met Glu Leu Leu Val Leu
165 170 175

Gly Thr Leu Glu Trp Arg Met Ile Ala Val Thr Pro Phe Pro Tyr Ile
180 185 190

Ser Tyr Phe Ala Ala Arg Phe Arg Glu Thr Ser Ala Gly Arg Ile Leu
195 200 205

Met Arg Ala Val Glu Cys Val Phe Ala Ala Ile Lys Val Ile Ser Ser
210 215 220

Val Glu Xaa Arg Pro Ser Thr Ile Ala Val Ala Ser Ile Leu
225 230 235

<210> 9
<211> 510
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (424)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (441)
<223> n = A, C, G or T

<400> 9
cttacagctt cctcctcgct ttgctggttg cagacgaacg cgggattccg gttcagcttg 60
aagacggcgt atgtcgcggt gacgtatctc gatcggttct tggcgcgccg gtgtgtcgat 120
agggacaagg agtgggcgct gcagctcctc tcggtggcgt gcctgtcgct ggcggcgaag 180
gtggaggagc gccggccgcc gcggctgccg gagttcaagc tggacatgta cgactgcgcg 240
tccttgatgc ggatggagct cctcgtcctc accacgctca agtggcagat gatcaccgag 300
acacccttct cctacctgaa ctgttcaccg cgaaattccg gcacgacgag cggaaggcat 360
cgtcctgcgc gccatcgaat gcatcttcgc tcgatcaaag tcatagctcg gtgggtacag 420
catnacgatc gctctagcag natctatcgt cggaacaagg agacggcgct aattagacga 480
ctaagtcgtc gtggctctat ggagcactaa 510

<210> 10
<211> 181
<212> PRT
<213> Oryza sativa

<400> 10
His Glu Leu Thr Ala Ser Ser Ser Leu Cys Trp Leu Gln Thr Asn Ala
1 5 10 15

Gly Phe Arg Phe Ser Leu Lys Thr Ala Tyr Val Ala Val Thr Tyr Leu
20 25 30

Asp Arg Phe Leu Ala Arg Arg Cys Val Asp Arg Asp Lys Glu Trp Ala
35 40 45

Leu Gln Leu Leu Ser Val Ala Cys Leu Ser Leu Ala Ala Lys Val Glu
50 55 60

Glu Arg Arg Pro Pro Arg Leu Pro Glu Phe Lys Leu Asp Met Tyr Asp
65 70 75 80

Cys Ala Ser Leu Met Arg Met Glu Leu Leu Val Leu Thr Thr Leu Lys
85 90 95

Trp Gln Met Ile Thr Glu Thr Pro Phe Ser Tyr Leu Asn Cys Phe Thr
100 105 110

Ala Lys Phe Arg His Asp Glu Arg Lys Ala Ile Val Leu Arg Ala Ile
115 120 125

Glu Cys Ile Phe Ala Ser Ile Lys Val Ile Ser Ser Val Gly Tyr Gln
130 135 140

Pro Ser Thr Ile Ala Leu Ala Ala Ile Leu Ile Ala Arg Asn Lys Glu
145 150 155 160

Thr Ala Pro Asn Leu Asp Glu Leu Ser Val His Arg Leu Ala Pro Trp
165 170 175

Gln Leu Met Met Leu
180

<210> 11
<211> 2259
<212> DNA
<213> Glycine max

<400> 11
acaacttctc ccactcattc atcaacaacc acacacactc tctctcccct ctctgcacca 60
aaaccacttc tccggcgaca tctccggtca ggttccggca acctcatcgg cgaatcggca 120
tgccaacaca atgaatgcgg aacctccgct gccgccggcg ctcctcatgt cggtttcctg 180
cctctccgac tacgacctcc tctgcggcga ggactcctcc ggaatcctct ccggagagtc 240
gccggagtgc tccttctccg acatcgactc ctcacctcct ccgccgtcgc cgacgacaga 300
ggattgttat tcgatcgcga gcttcatcga gcacgagcgc aacttcgttc cgggattcga 360
gtacctgtcg cggttccaat ctcgctccct ggacgccaac gccagagaag aatcagttgg 420
atggattctc aaggtacacg cgtactatgg ctttcagcct ttgacggcgt acctcgccgt 480
caactatatg gatcggtttt tggattctcg ccggttgccg gaaacaaatg ggtggcctct 540
gcaacttgta tctgttgcat gcttgtcttt ggcagcaaag atggaagaac ctcttgttcc 600
atctctcttg gaccttcaga tagaaggtgc caagtacata tttgagccga gaacaattcg 660
taggatggag ctacttgttc tcggtgtctt agattggagg ctaagatcag taacaccact 720
ttgcttcctc gctttctttg cgtgcaaagt agattcaact ggaactttta tccggttcct 780
tatttccagg gcaacagaaa tcatcgtatc taatatccaa gaggctagct ttcttgctta 840
ctggccttca tgcattgctg ctgcagccat actcactgca gctaatgaaa ttcctaattg 900
gtctgtggtt aagcccgaaa atgctgagtc atggtgcgag ggactaagaa aagaaaaagt 960
aatagggtgc taccagttga tgcaagagct tgtgattaac aataaccaac ggaaactccc 1020
cttactaaaa gtgttgccgc agctgcgagt aacaactcgg acccgaatga ggtcaagtac 1080
tgtatcatca ttctcatcat cctcttcaac ctccttctcc ttgtcttgta agaggaggaa 1140
attaaataac cgtttgtggg tagatgacaa aggaaactcc gagtgaagag aaaacgaaca 1200
acaataataa aagaagggaa gaaaaagaga gggaataagg tgggccaagt tgtctagaaa 1260
cctcaacatt ttttagaggg tttttgcaat taaaaaatga cttgagtgag ggtgtagatt 1320
ataatagtat atatatgata tatctctatc gtatatacta agagagtttg atgggtttgg 1380
agtaattttt atttttatgt tggtgactta ttaatattga gtttgcagaa ttcacctagg 1440
gaagagggat tttgcgacat gttaccgtgg gagaggaaat gagagaagaa agaagtgaaa 1500
cactgaacca ggggtagaag aatttaatgt gatttgttct tgtaacctgt gattctgaag 1560
gaaagaattg agttgcgggc tggatttcaa agtttgcatt aattacttgg tgaaggagat 1620
gaaagatggt gggggcaacg ctgtagagat tgagaagaag aaaaagtaga gagaaggtat 1680
gaaaaactct ggtgattatt gaaagttgaa acttagaagt ttgaagtgtt caatgttcat 1740
atcatggtat tcataagtca agcaaagctt catttcttgg ccagcatcac tgcttcttca 1800
tcatccacgt tactactact ttgatgggac cctcaacagt aaagaacaat tgaagggcaa 1860
taagttgaag tttggctaca aatcgtggac tttttttgtt gggtattggc acgtgtgcag 1920

tcggttctgg tgcgtgccaa tgaagtgtgt acgtgtgatt tttctttttc ttggtttttc 1980
tttgcgggag ctgtttatat atttttttcct atttttggcc atgagttttg gcctaactat 2040
acaggactcc aatggctggt gtccgcgcgt gtgatggaaa cacgtgtata tataggtttt 2100
aatttaaaaa ccttgaattt ttttatttgt tttcaagaga ggagaaccct ctttcacata 2160
ggggtaaaag gtctttgggg ccttttttcct gtgtgctgtg tattggattg attaatatat 2220
aatgacaact attaatttct taaaaaaaaa aaaaaaaaa 2259

<210> 12
<211> 339
<212> PRT
<213> Glycine max

<400> 12
Met Ser Val Ser Cys Leu Ser Asp Tyr Asp Leu Leu Cys Gly Glu Asp
1 5 10 15

Ser Ser Gly Ile Leu Ser Gly Glu Ser Pro Glu Cys Ser Phe Ser Asp
20 25 30

Ile Asp Ser Ser Pro Pro Pro Pro Ser Pro Thr Thr Glu Asp Cys Tyr
35 40 45

Ser Ile Ala Ser Phe Ile Glu His Glu Arg Asn Phe Val Pro Gly Phe
50 55 60

Glu Tyr Leu Ser Arg Phe Gln Ser Arg Ser Leu Asp Ala Asn Ala Arg
65 70 75 80

Glu Glu Ser Val Gly Trp Ile Leu Lys Val His Ala Tyr Tyr Gly Phe
85 90 95

Gln Pro Leu Thr Ala Tyr Leu Ala Val Asn Tyr Met Asp Arg Phe Leu
100 105 110

Asp Ser Arg Arg Leu Pro Glu Thr Asn Gly Trp Pro Leu Gln Leu Val
115 120 125

Ser Val Ala Cys Leu Ser Leu Ala Ala Lys Met Glu Glu Pro Leu Val
130 135 140

Pro Ser Leu Leu Asp Leu Gln Ile Glu Gly Ala Lys Tyr Ile Phe Glu
145 150 155 160

Pro Arg Thr Ile Arg Arg Met Glu Leu Leu Val Leu Gly Val Leu Asp
165 170 175

Trp Arg Leu Arg Ser Val Thr Pro Leu Cys Phe Leu Ala Phe Phe Ala
180 185 190

Cys Lys Val Asp Ser Thr Gly Thr Phe Ile Arg Phe Leu Ile Ser Arg
195 200 205

Ala Thr Glu Ile Ile Val Ser Asn Ile Gln Glu Ala Ser Phe Leu Ala
210 215 220

Tyr Trp Pro Ser Cys Ile Ala Ala Ala Ala Ile Leu Thr Ala Ala Asn
225 230 235 240

Glu Ile Pro Asn Trp Ser Val Val Lys Pro Glu Asn Ala Glu Ser Trp
245 250 255

Cys Glu Gly Leu Arg Lys Glu Lys Val Ile Gly Cys Tyr Gln Leu Met
260 265 270

Gln Glu Leu Val Ile Asn Asn Asn Gln Arg Lys Leu Pro Leu Leu Lys
275 280 285

Val Leu Pro Gln Leu Arg Val Thr Thr Arg Thr Arg Met Arg Ser Ser
290 295 300

Thr Val Ser Ser Phe Ser Ser Ser Ser Ser Thr Ser Phe Ser Leu Ser
305 310 315 320

Cys Lys Arg Arg Lys Leu Asn Asn Arg Leu Trp Val Asp Asp Lys Gly
325 330 335

Asn Ser Glu

<210> 13
<211> 1994
<212> DNA
<213> Glycine max

<400> 13
gcacgagccg gaatcatgga ttcctcgccg gagtgttcct ccgacctcga ttcctcgccg 60
ccgtcggagg cggagtccat cgccggattc atggaagacg agcgcaactt cgtccccgga 120
ttcgaatacc tcaataggtt ccaatctcgc tctctcgacg cctctgccag agaagaatcc 180
gttgcatgga ttctcaaggt gcaggcttat tacgcttttc aaccggtcac ggcttatctt 240
tccgttaact acttggatag gttcttgaat tctcgaccgt tgccgccgaa aacgaatggg 300
tggccactgc aacttctctc tgttgcgtgc ttgtctttag cagcaaagat ggaggaatct 360
ctagttccat ctcttttgga ccttcaggta gaaggtgcta aatacgtatt tgaacccaaa 420
acaattagaa gaatggagct acttgttctg ggcgtgttgg attggaggct aagatcggtt 480
accccattta gcttcctcga tttctttgcg tgcaagttag attcaactgg gacttttacc 540
gggttcctca tttcacgtgc tacacaaatt atcttatcta atatacaaga ggctagcttt 600
cttgcgtatt ggccatcatg cattgctgca gcagccattc tccatgcagc aaatgaaatt 660
cctaattggt ctctcgttag gcctgagcat gcagagtcat ggtgtgaggg gttaagaaag 720
gagaaaatta tagggtgcta ccaattaatg caagaacttg tgattgacaa taaccagagg 780
aaacccccta aggtgttacc acagctgcga gtgacaatat ctcggcccat tatgaggtct 840
agtgtctcat ccttcttagc atcatcctct tcaccttcat catcctcttt gtcttgtaga 900
aggaggaaat taaataactc tttgtgggta gacgatgaca aaggaaactc ccaatgaaga 960
gaaaaagaac aataatagag gaggaaaaaa agaagaataa tgaaataagg tggtggacgg 1020
tggtccaagt tgtccagaaa ccgcaaaatt tttaagaggg ttttttgag tataaaatgg 1080
actagagagt cgaggtgtac attataatat agactatatt ttatgagagt tgcgagcttt 1140
tattattttg ttggtgggtg ttgccattca tcaatggcat tgcagattcc ctagggaagg 1200
ggattttgca aagtgtgtgt gggtgtgcgt gagagagagg tgggaaatta gatacaaaga 1260
tgcatttaat ggtttggtcg tgcaagcgtg gaagaaagaa gtgtgtagtt tggaattcaa 1320
agatgcgctt gttattggtg aaagagaaga gaatggtggt gggacattgc ttcagagctt 1380
ggaagaagaa aaaaagcata gtctcagagc agatatcaat agggtattga aagactttga 1440
agtttgagct gtttcttctt attataatgg ggtctctaag tcaagctact catcttggcc 1500
agcatgcctc gcttcttcag tttacacgtt acttttggta gtgtgatggg ataccactag 1560
agtacaaaaa aagaaatagc aataaggtga atcttatcac attttgtgga cttatgatga 1620
tacgtgtgag acgcctctgg tgtgtgtctc gcacgtgcct acgtgtgatt ttttatttt 1680
atttatgttt tagctatggc gggaaatgct ttttatttct ttatttcttt tttggcttga 1740
gctttggcct aactatacag gatccattgc ctggtgtcca cgcgtgatgg aaacacgtgt 1800
ctatagtttt catttttgt tttggatttt ttcatttgtt ttcaagagag gagaaccctc 1860
ttttgttttc tttttagtgc ctaattggct ttgggagaaa ttggagtaaa ggcctttggg 1920
gccttttcct gagtgctttg tattgaattc attaataatg acactgttaa ttctataaaa 1980
aaaaaaaaaa aaaa 1994

<210> 14
<211> 318
<212> PRT
<213> Glycine max

<400> 14
Ala Arg Ala Gly Ile Met Asp Ser Ser Pro Glu Cys Ser Ser Asp Leu
1 5 10 15

Asp Ser Ser Pro Pro Ser Glu Ala Glu Ser Ile Ala Gly Phe Met Glu
20 25 30

```
Asp Glu Arg Asn Phe Val Pro Gly Phe Glu Tyr Leu Asn Arg Phe Gln
        35                  40                  45

Ser Arg Ser Leu Asp Ala Ser Ala Arg Glu Glu Ser Val Ala Trp Ile
    50                  55                  60

Leu Lys Val Gln Ala Tyr Tyr Ala Phe Gln Pro Val Thr Ala Tyr Leu
65                  70                  75                  80

Ser Val Asn Tyr Leu Asp Arg Phe Leu Asn Ser Arg Pro Leu Pro Pro
                85                  90                  95

Lys Thr Asn Gly Trp Pro Leu Gln Leu Leu Ser Val Ala Cys Leu Ser
            100                 105                 110

Leu Ala Ala Lys Met Glu Glu Ser Leu Val Pro Ser Leu Leu Asp Leu
        115                 120                 125

Gln Val Glu Gly Ala Lys Tyr Val Phe Glu Pro Lys Thr Ile Arg Arg
    130                 135                 140

Met Glu Leu Leu Val Leu Gly Val Leu Asp Trp Arg Leu Arg Ser Val
145                 150                 155                 160

Thr Pro Phe Ser Phe Leu Asp Phe Phe Ala Cys Lys Leu Asp Ser Thr
                165                 170                 175

Gly Thr Phe Thr Gly Phe Leu Ile Ser Arg Ala Thr Gln Ile Ile Leu
            180                 185                 190

Ser Asn Ile Gln Glu Ala Ser Phe Leu Ala Tyr Trp Pro Ser Cys Ile
        195                 200                 205

Ala Ala Ala Ala Ile Leu His Ala Ala Asn Glu Ile Pro Asn Trp Ser
    210                 215                 220

Leu Val Arg Pro Glu His Ala Glu Ser Trp Cys Glu Gly Leu Arg Lys
225                 230                 235                 240

Glu Lys Ile Ile Gly Cys Tyr Gln Leu Met Gln Glu Leu Val Ile Asp
                245                 250                 255

Asn Asn Gln Arg Lys Pro Pro Lys Val Leu Pro Gln Leu Arg Val Thr
            260                 265                 270

Ile Ser Arg Pro Ile Met Arg Ser Ser Val Ser Ser Phe Leu Ala Ser
        275                 280                 285

Ser Ser Ser Pro Ser Ser Ser Ser Leu Ser Cys Arg Arg Arg Lys Leu
    290                 295                 300

Asn Asn Ser Leu Trp Val Asp Asp Asp Lys Gly Asn Ser Gln
305                 310                 315

<210>  15
<211>  570
<212>  DNA
<213>  Triticum aestivum

<220>
<221>  unsure
<222>  (499)
<223>  n = A, C, G or T

<220>
<221>  unsure
```

<222> (515)..(516)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (558)
<223> n = A, C, G or T

<400> 15
acagaggttc acctaaaaaa aggctagcag ttcttcccaa agagacaaca gttctaagaa 60
aagaagcagg agctgcagct ggtgagcgtc tgtgccctgc tgattgcgtg caagtacgaa 120
gagatttggg ctccagaggt gaacgacttc atattgttct ccgacaacac atatactagg 180
gagcagattc tgaggatgga gaaggcaatc ctgaacatgc ttgagtggaa cctgacagtg 240
cccacacctt acgtcttcct cgtgtgattc gccaaggccg catcctcctg agataagaag 300
aacggcaagg aggtaaaagg aacaccagat tttaacaaat cctcagatgt agtacgtatc 360
tccatttgcc aaacatgatc tattgctgaa ttctgttctc cctggtgtat tgtctaaatg 420
gagacacgtc ttttttcgt ggactggcgc tctgtagtat ggacagaata tgtttgattc 480
agcacacaag agacaggtna tcaacacaca gtagnnacag tgtctgtaca gccgtataca 540
taacattata cttctcanag accactttgg 570

<210> 16
<211> 75
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (68)
<223> Xaa = ANY AMINO ACID

<400> 16
Lys Gln Glu Leu Gln Leu Val Ser Val Cys Ala Leu Leu Ile Ala Cys
1 5 10 15

Lys Tyr Glu Glu Ile Trp Ala Pro Glu Val Asn Asp Phe Ile Leu Phe
20 25 30

Ser Asp Asn Thr Tyr Thr Arg Glu Gln Ile Leu Arg Met Glu Lys Ala
35 40 45

Ile Leu Asn Met Leu Glu Trp Asn Leu Thr Val Pro Thr Pro Tyr Val
50 55 60

Phe Leu Val Xaa Phe Ala Lys Ala Ala Ser Ser
65 70 75

<210> 17
<211> 1932
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (8)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (26)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (159)
<223> n = A, C, G or T

<400> 17
gccacaantg caccgcagac sgcacntsgg cctccctcct ccgtccgtcc gtcctcttcc 60
ttgtgccttg tcctcctcca ctcgccactg ccgcattctg cccaagtccc aaacacgcgc 120
accagccacc cagcactcca gccgccagac cagagtctnc ggcgccgccg tcgcacgaca 180
ggagagggag agatacgcgg gctttgactt gccgccggtg cgtccgtgcg tgcctggtgg 240
gaatagtggg agacgccggt acagtacagg agccatggcg ccgagctgct acgacgcggc 300
agcgtccatg ctcctctgcg ccgaggagca cagcagcatc ctgtggtacg aggaggagga 360
ggaggagctg gaggcggtcg ggagaaggag cggccggtcg ccgggctacg gggacgactt 420
cggcgcggac ttgttcccgc cgcagtcgga ggaatgcgtg gccggtctgg tggagcggga 480
acgggaccac atgccggggc cgtgctacgg cgacaggctg cgcggcggcg gcggctgtct 540
ctgcgtccgc cgggaggccg tcgactggat ttggaaggct tacacgcacc acaggttccg 600
ccctctcact gcctacttgg cagtgaacta cctcgatcgc ttcctctcgc tgtctgaggt 660
gccggactgc aaggactgga tgacgcagct cctcgcggtg gcgtgcgttt ctctggccgc 720
caagatggag gaaaccgccg tcccgcagtg cctggacctt caggaggtcg gagacgcgcg 780
gtacgtgttc gaggcgaaga cggtccagag gatggagctc ctggttctaa caaccctcaa 840
ctggaggatg catgccgtga cgccgttctc ctacgtggat tacttcctga acaagctcaa 900
caacggcggc agcacggcgc cgaggagctg ctggctcttg cagtccgcgg agcttatctt 960
gcgtgcggcc agaggaaccg gctgcgtcgg gttcaggccg tccgagatcg ccgccgcggt 1020
tgcagccgcc gtggccggag acgtggacga cgcggacggc gtcgagaacg cctgctgcgc 1080
tcacgtagat aaggagcggg tgttgcggtg ccaggaagcg atcgggtcca tggcgtcctc 1140
ggcggccatt gacgacgcta ccgtgccacc gaaatctgcg agacgcagga gctcccccgt 1200
gcccgtgccg cagagccctg tgggggtgct ggacgcggct ccctgcctca gctacaggag 1260
cgaagaggca gcgactgcga ctgcgactgc gacttctgct gcctcacatg gggccctgg 1320
ctcttcaagc tcgtcctcga cctccccggt gaccagcaaa aggaggaaac tcgccagccg 1380
atgtgatgga tcgtgcagtg accggtcaaa gcgcgcgccc gcccaatgga ccaaagagtg 1440
aattgactag ggcgtctgct tgctttctga tcaaagagtg cattgagagg cggcaaaatg 1500
gaggaataaa ggggattttg gcatgacgag ggcaaaggag ttgatgaata aagacgcgac 1560
gaggtggaca acacctaaat tgccgatctt ttctttgcaa ggggagtagg ggacctgctt 1620
gggcctgggg gagggtagta gacagcccag cacaaaaacc tggttggtgt gccacgacca 1680
caatgggcgc gccagccatg gctttgtagg aaacacaagg gcgctagagg agatccgatg 1740
ggatgactca gaataaagat agtggaggga ccagaccgta tgcagtatgt gcaacaacta 1800
ggcactggca tgcttatgct caagtaatct gataacttga atgttgtgta tccgacaaac 1860
tgcttctgtg aagagagaaa tgcaggtaga cgatgaatgt atgtgaaaaa aaaaaaaaaa 1920
aaaaaaaaaa ac 1932

<210> 18
<211> 388
<212> PRT
<213> Zea mays

<400> 18
Met Ala Pro Ser Cys Tyr Asp Ala Ala Ala Ser Met Leu Leu Cys Ala
1 5 10 15

Glu Glu His Ser Ser Ile Leu Trp Tyr Glu Glu Glu Glu Glu Glu Leu
20 25 30

Glu Ala Val Gly Arg Arg Ser Gly Arg Ser Pro Gly Tyr Gly Asp Asp
35 40 45

Phe Gly Ala Asp Leu Phe Pro Pro Gln Ser Glu Glu Cys Val Ala Gly
50 55 60

Leu Val Glu Arg Glu Arg Asp His Met Pro Gly Pro Cys Tyr Gly Asp
65 70 75 80

Arg Leu Arg Gly Gly Gly Gly Cys Leu Cys Val Arg Arg Glu Ala Val
85 90 95

Asp Trp Ile Trp Lys Ala Tyr Thr His His Arg Phe Arg Pro Leu Thr
100 105 110

Ala Tyr Leu Ala Val Asn Tyr Leu Asp Arg Phe Leu Ser Leu Ser Glu
115 120 125

Val Pro Asp Cys Lys Asp Trp Met Thr Gln Leu Leu Ala Val Ala Cys
130 135 140

Val Ser Leu Ala Ala Lys Met Glu Glu Thr Ala Val Pro Gln Cys Leu
145 150 155 160

Asp Leu Gln Glu Val Gly Asp Ala Arg Tyr Val Phe Glu Ala Lys Thr
165 170 175

Val Gln Arg Met Glu Leu Leu Val Leu Thr Thr Leu Asn Trp Arg Met
180 185 190

His Ala Val Thr Pro Phe Ser Tyr Val Asp Tyr Phe Leu Asn Lys Leu
195 200 205

Asn Asn Gly Gly Ser Thr Ala Pro Arg Ser Cys Trp Leu Leu Gln Ser
210 215 220

Ala Glu Leu Ile Leu Arg Ala Ala Arg Gly Thr Gly Cys Val Gly Phe
225 230 235 240

Arg Pro Ser Glu Ile Ala Ala Ala Val Ala Ala Ala Val Ala Gly Asp
245 250 255

Val Asp Asp Ala Asp Gly Val Glu Asn Ala Cys Cys Ala His Val Asp
260 265 270

Lys Glu Arg Val Leu Arg Cys Gln Glu Ala Ile Gly Ser Met Ala Ser
275 280 285

Ser Ala Ala Ile Asp Asp Ala Thr Val Pro Pro Lys Ser Ala Arg Arg
290 295 300

Arg Ser Ser Pro Val Pro Val Pro Gln Ser Pro Val Gly Val Leu Asp
305 310 315 320

Ala Ala Pro Cys Leu Ser Tyr Arg Ser Glu Glu Ala Ala Thr Ala Thr
325 330 335

Ala Thr Ala Thr Ser Ala Ala Ser His Gly Ala Pro Gly Ser Ser Ser
340 345 350

Ser Ser Ser Thr Ser Pro Val Thr Ser Lys Arg Arg Lys Leu Ala Ser
355 360 365

Arg Cys Asp Gly Ser Cys Ser Asp Arg Ser Lys Arg Ala Pro Ala Gln
370 375 380

Trp Thr Lys Glu
385

<210> 19
<211> 481
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (88)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (130)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (251)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (311)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (352)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (359)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (394)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (400)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (408)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (410)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (415)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (420)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (426)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (432)..(433)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (448)
<223> n = A, C, G or T

<220>

<221> unsure
<222> (457)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (461)..(462)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (470)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (475)
<223> n = A, C, G or T

<400> 19
cttacatgta agctcgtgcc gaattcggca cgagcttaca cgagcgcaac ccatgggcgc 60
cgcggctgct cgccatcagc tgcctcancc tcgccgccaa gatgcagcgc gccgccgcca 120
tctccgccgn cgacatccag aggggcgagg agttcatgtt cgacgaggcg aaaatccagc 180
gcatggagca gatggtgctc aacgcgctgg agtggcggac gcgctccgtc acgccgctcg 240
ccttcctcgg nttctttctc tccgcgtggt tcccgcaagc cgcggcaccc ggcgctgctc 300
gatgccatca nggccgcgcc gtcgagctcc tcctccgcgt ctaagccggg angtgaacna 360
tggtgggagt tctccccctt cggtggccgg ccgncgcggn tctcctcncn gccgncggan 420
aaggcntccg gnngcccaaa ctccttcnct tccaaanctg nnggccccgn tttgnccccc 480
t 481

<210> 20
<211> 110
<212> PRT
<213> Oryza sativa
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (26)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (40)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (100)
<223> Xaa = ANY AMINO ACID

<400> 20
Ala Arg Ala Glu Phe Gly Thr Ser Leu His Glu Arg Asn Pro Trp Ala
1 5 10 15

Pro Arg Leu Leu Ala Ile Ser Cys Leu Xaa Leu Ala Ala Lys Met Gln
20 25 30

Arg Ala Ala Ala Ile Ser Ala Xaa Asp Ile Gln Arg Gly Glu Glu Phe
35 40 45

Met Phe Asp Glu Ala Lys Ile Gln Arg Met Glu Gln Met Val Leu Asn
50 55 60

Ala Leu Glu Trp Arg Thr Arg Ser Val Thr Pro Leu Ala Phe Leu Gly

65 70 75 80

Phe Phe Leu Ser Ala Trp Phe Pro Gln Ala Ala Ala Pro Gly Ala Ala
85 90 95

Arg Cys His Xaa Gly Arg Ala Val Glu Leu Leu Leu Arg Val
100 105 110

<210> 21
<211> 789
<212> DNA
<213> Triticum aestivum

<400> 21
cacctgaggg cgactcgagg gtgccctcgc cccgtccgcc gtgaccaccc ctcttcggat 60
ctcaccgcct cgaccaaaat gtgatttgag gcaaattctg cgtttgaggc aaggacaata 120
aaagtgatgg agcttttggt cttcagcacc ttgaaatgga ggatgcaagc tgttactgct 180
tgctcgttta ttgactactt cctttgcaaa ttcaatgatc atgacacacc ctccatgctt 240
gcattctcct gctcaactga cctcatcctg agcacaacta agtgagctga ttttttggtg 300
ttcagacatt cagagattgc tggaagtgtt gcacttcctt catttgggga gcacaagact 360
tcagttgtcg aaatggctac aactaattgc aagtatataa acaagggagt gtgatgtgac 420
aggaaagatc ctgatgaagt gcttccttta tggaatgcct atctgaagtt tggactaaga 480
gacatgcttt aattggctta gtaaaaaata cttgctaaag agaaataaga ttcaaagtag 540
atgtttttat tgtagattag gatatgtgtg ttctgccacc ggttcgactt ctcatattag 600
aaggcaagca gttagttcat atcttactac tttgcactat tgtagatgga tggtgaggga 660
ttgagaggct actactatta atgtgcgtaa actttgcatc tttagctctc taaatgaaac 720
cggtgatggt taacctgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780
aaaaaaaaa 789

<210> 22
<211> 163
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (28)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (95)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (138)
<223> Xaa = ANY AMINO ACID

<400> 22
His Leu Arg Ala Thr Arg Gly Cys Pro Arg Pro Val Arg Arg Asp His
1 5 10 15

Pro Ser Ser Asp Leu Thr Ala Ser Thr Lys Met Xaa Phe Glu Ala Asn
20 25 30

Ser Ala Phe Glu Ala Arg Thr Ile Lys Val Met Glu Leu Leu Val Phe
35 40 45

Ser Thr Leu Lys Trp Arg Met Gln Ala Val Thr Ala Cys Ser Phe Ile
50 55 60

Asp Tyr Phe Leu Cys Lys Phe Asn Asp His Asp Thr Pro Ser Met Leu
65 70 75 80

Ala Phe Ser Cys Ser Thr Asp Leu Ile Leu Ser Thr Thr Lys Xaa Ala
85 90 95

Asp Phe Leu Val Phe Arg His Ser Glu Ile Ala Gly Ser Val Ala Leu
100 105 110

Pro Ser Phe Gly Glu His Lys Thr Ser Val Val Glu Met Ala Thr Thr
115 120 125

Asn Cys Lys Tyr Ile Asn Lys Gly Val Xaa Cys Asp Arg Lys Asp Pro
130 135 140

Asp Glu Val Leu Pro Leu Trp Asn Ala Tyr Leu Lys Phe Gly Leu Arg
145 150 155 160

Asp Met Leu

<210> 23
<211> 1132
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (441)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (447)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (485)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (498)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (528)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (553)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (560)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (576)..(577)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (598)

<223> n = A, C, G or T

<220>
<221> unsure
<222> (1126)
<223> n = A, C, G or T

<400> 23
aacagaattc ggcacgagcc gcggtcggct gggtttcacg cgccgcggcg cggctaggct 60
tctccgcgct caccgccgcg ctcgccgccg cctacctcga ccgctgcttc ctccccgggg 120
gcgcgctccg gctcggcgac cagccctgga tggcgcgcct agccgccgtc acctgcttcg 180
cgctcgccgc caaggtcgag gagacgcgcg tgccgccgct cctcgacctc cagctctacg 240
ccgccgctga cgccgcggat ccgtacgtat tcgaggccaa gacggtgcgc cggatggagc 300
tgctcgtgct ctccgcgctt gggtggcgga tgcaccctgt cacgcccttc tcctacctcc 360
agcccgtcct cgccgacgct gcgacgcgcc tgcgtagctg cgagggcgtc ctgctcgcgg 420
tcatggccga ctggaggtgg cctcggcacc ggccttcggc gtgggccgcc gccgcgttgc 480
tgatcacagc cgccgccggc gacggcggcg acggcgacgg cgacacggag ctcctggcgc 540
tcatcaatgc ccccgaggac aagaccgccg agtgtgccaa gatcatctcc gaggtgacgg 600
gcatgagctt cctcgcctgc gatgtcggcg tgagcgccgg aaataagcgt aagcacgcgg 660
cggcgcagtt gtactcgccg ccgccgagcc cgagcggcgt gatcggcgcg ctgtcctgct 720
tcagctgcga gagctcgacg tccgccaccg ctatggctgc ggcggtcggc ccgtgggcgc 780
cgtcggcgtc cgtgtccgtg tcgtcctctc cagagccacc aggtcgggcc cccaagcgcg 840
cagcggcggc gtcggcgtcg gcgtcggcgt cagccggggt cgcgccaccg gtccaggtcc 900
cgcatcagct acccccccgac gaggagagcc gcgacgcctg gccgtccacc tgcgccgcgt 960
gacgcaccgt gccggaaacg gtgcctatgg cgagaccgcc gttcggtggc ggtggagaat 1020
ggagaacaag gagcatcatt ggctcgcgtc ggtgagcagg agaacgaact attttgccca 1080
ttgccgtgac agatgggggg tgttcactgc gtggagccgc gctgancaat ga 1132

<210> 24
<211> 318
<212> PRT
<213> Zea mays

<400> 24
Asn Ser Ala Arg Ala Ala Val Gly Trp Val Ser Arg Ala Ala Ala Arg
1 5 10 15

Leu Gly Phe Ser Ala Leu Thr Ala Ala Leu Ala Ala Ala Tyr Leu Asp
20 25 30

Arg Cys Phe Leu Pro Gly Gly Ala Leu Arg Leu Gly Asp Gln Pro Trp
35 40 45

Met Ala Arg Leu Ala Ala Val Thr Cys Phe Ala Leu Ala Ala Lys Val
50 55 60

Glu Glu Thr Arg Val Pro Pro Leu Leu Asp Leu Gln Leu Tyr Ala Ala
65 70 75 80

Ala Asp Ala Ala Asp Pro Tyr Val Phe Glu Ala Lys Thr Val Arg Arg
85 90 95

Met Glu Leu Leu Val Leu Ser Ala Leu Gly Trp Arg Met His Pro Val
100 105 110

Thr Pro Phe Ser Tyr Leu Gln Pro Val Leu Ala Asp Ala Ala Thr Arg
115 120 125

Leu Arg Ser Cys Glu Gly Val Leu Leu Ala Val Met Ala Asp Trp Arg
130 135 140

Trp Pro Arg His Arg Pro Ser Ala Trp Ala Ala Ala Ala Leu Leu Ile
145 150 155 160

Thr Ala Ala Ala Gly Asp Gly Gly Asp Gly Asp Gly Asp Thr Glu Leu
165 170 175

Leu Ala Leu Ile Asn Ala Pro Glu Asp Lys Thr Ala Glu Cys Ala Lys
180 185 190

Ile Ile Ser Glu Val Thr Gly Met Ser Phe Leu Ala Cys Asp Val Gly
195 200 205

Val Ser Ala Gly Asn Lys Arg Lys His Ala Ala Ala Gln Leu Tyr Ser
210 215 220

Pro Pro Pro Ser Pro Ser Gly Val Ile Gly Ala Leu Ser Cys Phe Ser
225 230 235 240

Cys Glu Ser Ser Thr Ser Ala Thr Ala Met Ala Ala Ala Val Gly Pro
245 250 255

Trp Ala Pro Ser Ala Ser Val Ser Val Ser Ser Ser Pro Glu Pro Pro
260 265 270

Gly Arg Ala Pro Lys Arg Ala Ala Ala Ala Ser Ala Ser Ala Ser Ala
275 280 285

Ser Ala Gly Val Ala Pro Pro Val Gln Val Pro His Gln Leu Pro Pro
290 295 300

Asp Glu Glu Ser Arg Asp Ala Trp Pro Ser Thr Cys Ala Ala
305 310 315

<210> 25
<211> 674
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (527)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (561)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (640)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (643)
<223> n = A, C, G or T

<400> 25
cactcactca ccccttcctt tctaactcct caaattgtgt gttctgagaa tggaaatgcc 60
tccttctcca tcggggcatt ccgcactctc catcccataa aagtcccaga tccaagatgg 120
cttaccacca tcaaaaatcc cttttggaca ccctatactg ctccgaagag cattggatag 180
gggaaggtga atttgaccaa gcagaggagg agtacggtaa cagtaatagc aatagtagca 240
gcaccttagt aaacaactcc cctgagtcct cccctcattt gttgctcgaa agcgacatgt 300
tttgggacga acaagagttg gcatcgctgt tggagaaaga acaacacaac ccactaagca 360
cttgctgtct ccaaagcaac cctgccttgg agggtgctcg catagaagcc gtggagtgga 420
ttctcaaagt aaacgcccac tactccttct ctgccctcac cgctgttctt gctgtcaact 480
actttgaccg ttttctcttc agcttccgct ttcagaatga cattaancca tggatgactc 540
ggggtcgctg ccgtcgcttg nctctccctc gctgccaaag tgggcgagac acacgttccc 600
tttcttattt gacccttcaa caaagtggga ggaggagtan atnctttgtt ccaagccaaa 660
gacgattaaa aaag 674

<210> 26
<211> 186
<212> PRT
<213> Glycine max
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (137)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (149)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (175)..(176)
<223> Xaa = ANY AMINO ACID

<400> 26

```
Met Ala Tyr His His Gln Lys Ser Leu Leu Asp Thr Leu Tyr Cys Ser
1               5                  10                  15

Glu Glu His Trp Ile Gly Glu Gly Glu Phe Asp Gln Ala Glu Glu Glu
            20                  25                  30

Tyr Gly Asn Ser Asn Ser Asn Ser Ser Ser Thr Leu Val Asn Asn Ser
        35                  40                  45

Pro Glu Ser Ser Pro His Leu Leu Leu Glu Ser Asp Met Phe Trp Asp
    50                  55                  60

Glu Gln Glu Leu Ala Ser Leu Leu Glu Lys Glu Gln His Asn Pro Leu
65                  70                  75                  80

Ser Thr Cys Cys Leu Gln Ser Asn Pro Ala Leu Glu Gly Ala Arg Ile
                85                  90                  95

Glu Ala Val Glu Trp Ile Leu Lys Val Asn Ala His Tyr Ser Phe Ser
            100                 105                 110

Ala Leu Thr Ala Val Leu Ala Val Asn Tyr Phe Asp Arg Phe Leu Phe
        115                 120                 125

Ser Phe Arg Phe Gln Asn Asp Ile Xaa Pro Trp Met Thr Arg Gly Arg
    130                 135                 140

Cys Arg Arg Leu Xaa Leu Pro Arg Cys Gln Ser Gly Arg Asp Thr Arg
145                 150                 155                 160

Ser Leu Ser Tyr Leu Thr Leu Gln Gln Ser Gly Arg Arg Ser Xaa Xaa
                165                 170                 175

Phe Val Pro Ser Gln Arg Arg Leu Lys Lys
            180                 185
```

<210> 27
<211> 554
<212> DNA
<213> Glycine max

<400> 27

ctccctttca cctttcttca tagcctacca cttttctgct ttcatctact ctcacttctc 60
ttcacacact gagacacaca gagagagaaa aataaagggt gtgatgggtg tcttactgag 120
tgttttcttt ttataatgaa caaagaactg cacaccctct tcttcaccga agaagaagat 180
ggcaattcag caccacaatg accaactaga gcataatgaa aatgtctcat ctgtccttga 240
tgcccttac tgtgacgaag gaaagtggga agaggaagag gaggagaaag aagaagaaga 300
agatgaaggt gaaaatgaaa gtgaagtgac aacaaacact gcaacttgtc ttttccctct 360
gctcttgttg gagcaagact tgttctggga agatgaggaa ctaaactcta tcttttccaa 420
agagaaggtt caacatgaag aagcctatgg tataacaatc tgaacagtga tgtgtataac 480
aacaacaaca atactagtat ataatgtgat ttggctcttg ctcttcagct cgtcggagcg 540
tgatgatgct gaat 554

<210> 28
<211> 94
<212> PRT
<213> Glycine max

<400> 28
Met Ala Ile Gln His His Asn Asp Gln Leu Glu His Asn Glu Asn Val
1 5 10 15

Ser Ser Val Leu Asp Ala Leu Tyr Cys Asp Glu Gly Lys Trp Glu Glu
20 25 30

Glu Glu Glu Glu Lys Glu Glu Glu Glu Asp Glu Gly Glu Asn Glu Ser
35 40 45

Glu Val Thr Thr Asn Thr Ala Thr Cys Leu Phe Pro Leu Leu Leu Leu
50 55 60

Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Asn Ser Ile Phe Ser
65 70 75 80

Lys Glu Lys Val Gln His Glu Glu Ala Tyr Gly Ile Thr Ile
85 90

<210> 29
<211> 372
<212> PRT
<213> Catharanthus roseus

<400> 29
Met Ala Asp Lys Glu Asn Cys Ile Arg Val Thr Arg Leu Ala Lys Lys
1 5 10 15

Arg Ala Val Glu Ala Met Ala Ala Ser Glu Gln Gln Arg Pro Ser Lys
20 25 30

Lys Arg Val Val Leu Gly Glu Leu Lys Asn Leu Ser Ser Asn Ile Ser
35 40 45

Ser Ile Gln Thr Tyr Asp Phe Ser Ser Gly Pro Gln Lys Gln Gln Lys
50 55 60

Asn Lys Asn Lys Arg Lys Ala Lys Glu Ser Leu Gly Phe Glu Val Lys
65 70 75 80

Glu Lys Lys Val Glu Glu Ala Gly Ile Asp Val Phe Ser Gln Ser Asp
85 90 95

Asp Pro Gln Met Cys Gly Ala Tyr Val Ser Asp Ile Tyr Glu Tyr Leu
100 105 110

His Lys Met Glu Met Glu Thr Lys Arg Arg Pro Leu Pro Asp Tyr Leu
115 120 125

Asp Lys Val Gln Lys Asp Val Thr Ala Asn Met Arg Gly Val Leu Ile

130 135 140

Asp Trp Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Leu Pro Asp Thr
145 150 155 160

Leu Tyr Leu Thr Val Ser Tyr Ile Asp Arg Phe Leu Ser Met Asn Ala
165 170 175

Leu Ser Arg Gln Lys Leu Gln Leu Leu Gly Val Ser Ser Met Leu Ile
180 185 190

Ala Ser Lys Tyr Glu Glu Ile Ser Pro Pro His Val Glu Asp Phe Cys
195 200 205

Tyr Ile Thr Asp Asn Thr Tyr Lys Lys Glu Glu Val Val Lys Met Glu
210 215 220

Ala Asp Val Leu Lys Phe Leu Lys Phe Glu Met Gly Asn Pro Thr Ile
225 230 235 240

Lys Thr Phe Leu Arg Arg Leu Thr Arg Val Val Gln Asp Gly Asp Lys
245 250 255

Asn Pro Asn Leu Gln Phe Glu Phe Leu Gly Tyr Tyr Leu Ala Glu Leu
260 265 270

Ser Leu Leu Asp Tyr Gly Cys Val Lys Phe Leu Pro Ser Leu Ile Ala
275 280 285

Ser Ser Val Ile Phe Leu Ser Arg Phe Thr Leu Gln Pro Lys Val His
290 295 300

Pro Trp Asn Ser Leu Leu Gln His Asn Ser Gly Tyr Lys Pro Ala Asp
305 310 315 320

Leu Lys Glu Cys Val Leu Ile Ile His Asp Leu Gln Leu Ser Lys Arg
325 330 335

Gly Ser Ser Leu Val Ala Val Arg Asp Lys Tyr Lys Gln His Lys Phe
340 345 350

Lys Cys Val Ser Thr Leu Thr Ala Pro Pro Ser Ile Pro Asp Glu Phe
355 360 365

Phe Glu Asp Ile
370

<210> 30
<211> 335
<212> PRT
<213> Arabidopsis thaliana

<400> 30
Met Arg Ser Tyr Arg Phe Ser Asp Tyr Leu His Met Ser Val Ser Phe
1 5 10 15

Ser Asn Asp Met Asp Leu Phe Cys Gly Glu Asp Ser Gly Val Phe Ser
20 25 30

Gly Glu Ser Thr Val Asp Phe Ser Ser Ser Glu Val Asp Ser Trp Pro
35 40 45

Gly Asp Ser Ile Ala Cys Phe Ile Glu Asp Glu Arg His Phe Val Pro
50 55 60

Gly His Asp Tyr Leu Ser Arg Phe Gln Thr Arg Ser Leu Asp Ala Ser

65 70 75 80

Ala Arg Glu Asp Ser Val Ala Trp Ile Leu Lys Val Gln Ala Tyr Tyr
85 90 95

Asn Phe Gln Pro Leu Thr Ala Tyr Leu Ala Val Asn Tyr Met Asp Arg
100 105 110

Phe Leu Tyr Ala Arg Arg Leu Pro Glu Thr Ser Gly Trp Pro Met Gln
115 120 125

Leu Leu Ala Val Ala Cys Leu Ser Leu Ala Ala Lys Met Glu Glu Ile
130 135 140

Leu Val Pro Ser Leu Phe Asp Phe Gln Val Ala Gly Val Lys Tyr Leu
145 150 155 160

Phe Glu Ala Lys Thr Ile Lys Arg Met Glu Leu Leu Val Leu Ser Val
165 170 175

Leu Asp Trp Arg Leu Arg Ser Val Thr Pro Phe Asp Phe Ile Ser Phe
180 185 190

Phe Ala Tyr Lys Ile Asp Pro Ser Gly Thr Phe Leu Gly Phe Phe Ile
195 200 205

Ser His Ala Thr Glu Ile Ile Leu Ser Asn Ile Lys Glu Ala Ser Phe
210 215 220

Leu Glu Tyr Trp Pro Ser Ser Ile Ala Ala Ala Ala Ile Leu Cys Val
225 230 235 240

Ala Asn Glu Leu Pro Ser Leu Ser Ser Val Val Asn Pro His Glu Ser
245 250 255

Pro Glu Thr Trp Cys Asp Gly Leu Ser Lys Glu Lys Ile Val Arg Cys
260 265 270

Tyr Arg Leu Met Lys Ala Met Ala Ile Glu Asn Asn Arg Leu Asn Thr
275 280 285

Pro Lys Val Ile Ala Lys Leu Arg Val Ser Val Arg Ala Ser Ser Thr
290 295 300

Leu Thr Arg Pro Ser Asp Glu Ser Ser Ser Pro Cys Lys Arg Arg Lys
305 310 315 320

Leu Ser Gly Tyr Ser Trp Val Gly Asp Glu Thr Ser Thr Ser Asn
325 330 335

<210> 31
<211> 354
<212> PRT
<213> Nicotiana tabacum

<400> 31
Met Ala Ala Asp Asn Ile Tyr Asp Phe Val Ala Ser Asn Leu Leu Cys
1 5 10 15

Thr Glu Thr Lys Ser Leu Cys Phe Asp Asp Val Asp Ser Leu Thr Ile
20 25 30

Ser Gln Gln Asn Ile Glu Thr Lys Ser Lys Asp Leu Ser Phe Asn Asn
35 40 45

Gly Ile Arg Ser Glu Pro Leu Ile Asp Leu Pro Ser Leu Ser Glu Glu

50 55 60

Cys Leu Ser Phe Met Val Gln Arg Glu Met Glu Phe Leu Pro Lys Asp
65 70 75 80

Asp Tyr Val Glu Arg Leu Arg Ser Gly Asp Leu Asp Leu Ser Val Arg
85 90 95

Lys Glu Ala Leu Asp Trp Ile Leu Lys Ala His Met His Tyr Gly Phe
100 105 110

Gly Glu Leu Ser Phe Cys Leu Ser Ile Asn Tyr Leu Asp Arg Phe Leu
115 120 125

Ser Leu Tyr Glu Leu Pro Arg Ser Lys Thr Trp Thr Val Gln Leu Leu
130 135 140

Ala Val Ala Cys Leu Ser Leu Ala Ala Lys Met Glu Glu Ile Asn Val
145 150 155 160

Pro Leu Thr Val Asp Leu Gln Val Gly Asp Pro Lys Phe Val Phe Glu
165 170 175

Gly Lys Thr Ile Gln Arg Met Glu Leu Leu Val Leu Ser Thr Leu Lys
180 185 190

Trp Arg Met Gln Ala Tyr Thr Pro Tyr Thr Phe Ile Asp Tyr Phe Met
195 200 205

Arg Lys Met Asn Gly Asp Gln Ile Pro Ser Arg Pro Leu Ile Ser Gly
210 215 220

Ser Met Gln Leu Ile Leu Ser Ile Ile Arg Ser Ile Asp Phe Leu Glu
225 230 235 240

Phe Arg Ser Ser Glu Ile Ala Ala Ser Val Ala Met Ser Val Ser Gly
245 250 255

Glu Ile Gln Ala Lys Asp Ile Asp Lys Ala Met Pro Cys Phe Phe Ile
260 265 270

His Leu Asp Lys Gly Arg Val Gln Lys Cys Val Glu Leu Ile Gln Asp
275 280 285

Leu Thr Thr Ala Thr Ile Thr Thr Ala Ala Ala Ala Ser Leu Val Pro
290 295 300

Gln Ser Pro Ile Gly Val Leu Glu Ala Ala Ala Cys Leu Ser Tyr Lys
305 310 315 320

Ser Gly Asp Glu Arg Thr Val Gly Ser Cys Thr Thr Ser Ser His Thr
325 330 335

Lys Arg Arg Lys Leu Asp Thr Ser Ser Leu Glu His Gly Thr Ser Glu
340 345 350

Lys Leu

<210> 32
<211> 373
<212> PRT
<213> Nicotiana tabacum

<400> 32
Met Ala Ile Glu His Asn Glu Gln Gln Glu Leu Ser Gln Ser Phe Leu

1 5 10 15

Leu Asp Ala Leu Tyr Cys Glu Glu Glu Glu Glu Lys Trp Gly Asp Leu
20 25 30

Val Asp Asp Glu Thr Ile Ile Thr Pro Leu Ser Ser Glu Val Thr Thr
35 40 45

Thr Thr Thr Thr Thr Thr Lys Pro Asn Ser Leu Leu Pro Leu Leu Leu
50 55 60

Leu Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Leu Ser Leu Phe
65 70 75 80

Ser Lys Glu Lys Glu Thr His Cys Trp Phe Asn Ser Phe Gln Asp Asp
85 90 95

Ser Leu Leu Cys Ser Ala Arg Val Asp Ser Val Glu Trp Ile Leu Lys
100 105 110

Val Asn Gly Tyr Tyr Gly Phe Ser Ala Leu Thr Ala Val Leu Ala Ile
115 120 125

Asn Tyr Phe Asp Arg Phe Leu Thr Ser Leu His Tyr Gln Lys Asp Lys
130 135 140

Pro Trp Met Ile Gln Leu Ala Ala Val Thr Cys Leu Ser Leu Ala Ala
145 150 155 160

Lys Val Glu Glu Thr Gln Val Pro Leu Leu Leu Asp Phe Gln Val Glu
165 170 175

Asp Ala Lys Tyr Val Phe Glu Ala Lys Thr Ile Gln Arg Met Glu Leu
180 185 190

Leu Val Leu Ser Ser Leu Lys Trp Arg Met Asn Pro Val Thr Pro Leu
195 200 205

Ser Phe Leu Asp His Ile Ile Arg Arg Leu Gly Leu Arg Asn Asn Ile
210 215 220

His Trp Glu Phe Leu Arg Arg Cys Glu Asn Leu Leu Leu Ser Ile Met
225 230 235 240

Ala Asp Cys Arg Phe Val Arg Tyr Met Pro Ser Val Leu Ala Thr Ala
245 250 255

Ile Met Leu His Val Ile His Gln Val Glu Pro Cys Asn Ser Val Asp
260 265 270

Tyr Gln Asn Gln Leu Leu Gly Val Leu Lys Ile Asn Lys Glu Lys Val
275 280 285

Asn Asn Cys Phe Glu Leu Ile Ser Glu Val Cys Ser Lys Pro Ile Ser
290 295 300

His Lys Arg Lys Tyr Glu Asn Pro Ser His Ser Pro Ser Gly Val Ile
305 310 315 320

Asp Pro Ile Tyr Ser Ser Glu Ser Ser Asn Asp Ser Trp Asp Leu Glu
325 330 335

Ser Thr Ser Ser Tyr Phe Pro Val Phe Lys Lys Ser Arg Val Gln Glu
340 345 350

Gln Gln Met Lys Leu Ala Ser Ser Ile Ser Arg Val Phe Val Glu Ala

355 360 365

Val Gly Ser Pro His
370